



Initial Score = 9 Optimized Score = 15 Significance = -0.52  
Residue Identity = 51% Matches = 15 Mismatches = 14  
Gaps = 0 Conservative Substitutions = 0

1380 1390 1400 1410 1420 1430 1440  
CGTTTGACCATCTCGTCTGATATTAGCAAAATAATTTATATGTGGCCGGTTTCGTTAATACGGCA  
||| ||| ||| ||| |||  
GCCATATGAAATAATTTATTTAGAGTG  
X 10 20 X

26. US-08-816-977-48 (1-2085)  
US-08-816-977-14 Sequence 14, Application US/08816977

Initial Score = 8 Optimized Score = 13 Significance = -0.52  
Residue Identity = 46% Matches = 13 Mismatches = 15  
Gaps = 0 Conservative Substitutions = 0

500 510 520 530 540 X 550 560  
GGGGTTATGCGTTCAAGTATGAAAGCGCAAGTACGACATTAAAGACGTGGCGGTGGATAACGCTGG  
| | | | |  
GCCATATGAAATAATTTATTTAGAGTG  
X 10 20 X

28. US-08-816-977-48 (1-2085)  
US-08-816-977-15 Sequence 15, Application US/08816977

Initial Score = 8 Optimized Score = 14 Significance = -0.52  
Residue Identity = 48% Matches = 14 Mismatches = 15  
Gaps = 0 Conservative Substitutions = 0

1970 1980 1990 2000 2010 2020 2030  
ATGTCAGATAACTGGCGCAGCGCTGTTATAAAATAACAATACATTTATGGAAAGTAAATACAGCTGC  
||| | ||| ||| |  
GGCTCGAGACGAAATAACTTCGCTGAA  
X 10 20 X

29. US-08-816-977-48 (1-2085)  
US-08-816-977-17 Sequence 17, Application US/08816977

Initial Score = 8 Optimized Score = 13 Significance = -0.52  
Residue Identity = 43% Matches = 13 Mismatches = 17  
Gaps = 0 Conservative Substitutions = 0

1960 1970 X 1980 1990 2000 X 2010 2020  
GAGAGTCAACCAAGATGTCAGATAACTGGCGCAGCGCTGTTATAAAATAACAATACATTTATGGGAAA  
| | | | |  
GGCTCGAGTTTACCCGTTGTATATAAAAC  
X 10 20 30

31. US-08-816-977-48 (1-2085)  
US-08-816-977-18 Sequence 18, Application US/08816977

Initial Score = 7 Optimized Score = 12 Significance = -0.52  
Residue Identity = 46% Matches = 12 Mismatches = 14  
Gaps = 0 Conservative Substitutions = 0

1930 1940 1950 1960 1970 1980  
CAGGGGCGCGTCTGTTCCGCGGTGAATGAAGAGAGTCAACCAAGATGTCAGATAACGGCGAC  
||| | ||| |  
CGCATATGAAGAGAGATGTTATGGCG  
X 10 20 X



Initial Score = 9 Optimized Score = 13 Significance = -0.59  
Residue Identity = 50% Matches = 13 Mismatches = 13  
Gaps = 0 Conservative Substitutions = 0

1870 1880 1890 1900 1910 1920 1930  
AGCGTAGCCACCAAGCGTGTGTCGCCAGAGATAATGTCAGGGCCATCGCCAGTTGCCGCAAC  
||| ||||| |||  
CGCATATGAGAGAGATGTTTATGGCG  
X 10 20 X

26. US-08-816-977-48' (1-2085)  
US-08-816-977-15 Sequence 15, Application US/08816977

Initial Score = 9 Optimized Score = 13 Significance = -0.59  
Residue Identity = 44% Matches = 13 Mismatches = 16  
Gaps = 0 Conservative Substitutions = 0

720 730 740 750 760 770 780  
CATAGACATCAAGCCCTCGTATATCCACAGCAAAATAACTGCCCGGGGTGTTTAAACAGAC  
| ||||| |||  
GGCTCGAGACGAAATAACTTCGCTGAA  
X 10 20 X

27. US-08-816-977-48' (1-2085)  
US-08-816-977-12 Sequence 12, Application US/08816977

Initial Score = 9 Optimized Score = 17 Significance = -0.59  
Residue Identity = 58% Matches = 17 Mismatches = 12  
Gaps = 0 Conservative Substitutions = 0

50 60 70 80 90 100 110  
CGCTGCAGCTGATTACTTTCCCATATGATTGTTTATTTTATAACAGGCCTGCGCAGTTATCTG  
||||| || ||||| |||  
GCCATATGAAATAATTTATTTTAGAGTG  
X 10 20 X

30. US-08-816-977-48' (1-2085)  
US-08-816-977-14 Sequence 14, Application US/08816977

Initial Score = 8 Optimized Score = 14 Significance = -0.89  
Residue Identity = 50% Matches = 14 Mismatches = 14  
Gaps = 0 Conservative Substitutions = 0

10 20 30 40 50  
TTATTTACCCGTTGATATAAAACTGTGACTTTCTGTTTCAGAAACGCTGCAGCT  
||| ||||| |||  
GCCATATGAAATAACATTATTAATAGC  
X 10 20 X

34. US-08-816-977-48' (1-2085)  
US-08-816-977-13 Sequence 13, Application US/08816977

Initial Score = 7 Optimized Score = 11 Significance = -1.19  
Residue Identity = 37% Matches = 11 Mismatches = 18  
Gaps = 0 Conservative Substitutions = 0

1410 1420 1430 1440 1450 1460 1470  
GGTCATCGCTGTTTCGCTTTATTAAGGAGCTTCTGCGATGGAGTAATCGGTGTCGATTCAATG  
||| ||||| |||  
GGCTCGAGAGCTGCTAATAGTTCTGCGCAT  
X 10 20 X